



Exhibit C
BLAST result of SEQ ID NO:1 v rsus human genome

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Database: Homo_sapiens.latestgp.masked.fa
33,840 sequences; 200,810,911,373 total letters

Query= LEX181seqid1
(1395 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AL133463.16.1.84122	1030	0.0
AL050320.19.1.107057	363	1e-97

>AL133463.16.1.84122
Length = 84122

Score = 1030 bits (519), Expect = 0.0

Identities = 519/519 (100%)

Strand = Plus / Plus

Query: 877 gacacagacagctgtgagcgctggatgagctgcaaaagcgagttcttaaagaagtacatg 936
|||||
Sbjct: 28357 gacacagacagctgtgagcgctggatgagctgcaaaagcgagttcttaaagaagtacatg
28416

Query: 937 cacaaggatgaatgacctgccagctgcccctgctcctacccactgaggtggcctac 996
|||||
Sbjct: 28417 cacaaggatgaatgacctgccagctgcccctgctcctacccactgaggtggcctac
28476

Query: 997 agcacggccgacatcttcgaccgcatcaagcgcaaggacttccgctggaaggacgccagc
1056
|||||
Sbjct: 28477 agcacggccgacatcttcgaccgcatcaagcgcaaggacttccgctggaaggacgccagc
28536

Query: 1057 gggcccaaggagaagctggagatctacaagcccactgcccgggtactgcatccgctccatg
1116
|||||
Sbjct: 28537 gggcccaaggagaagctggagatctacaagcccactgcccgggtactgcatccgctccatg
28596

Query: 616 tttgaaaccaaagatcagccagaatatg 643
|||||
Sbjct: 9287 tttgaaaccaaagatcagccagaatatg 9314

Score = 312 bits (157), Expect = 5e-82
Identities = 159/161 (98%)
Strand = Plus / Plus

Query: 220 caccaggctgcacaccaacccttccccagaccgcgattccgacaagagacggggcacct 279
|||||
Sbjct: 1 caccaggctgcacaccaacccttccccagaccgcgattccgacaagagacggggcacct 60

Query: 280 tcattgcaaagagatttccccagatcctttctccttgatctaccaaactttccagatctt 339
|||||
Sbjct: 61 tcattgcaaagagatttccccagatcctttctccttgatctaccaaactttccagatctt 120

Query: 340 tccaaagctgatatcaatgggcagrwttccaaatatccaggt 380
|||||
Sbjct: 121 tccaaagctgatatcaatgggcagaatccaaatatccaggt 161

Score = 290 bits (146), Expect = 2e-75
Identities = 146/146 (100%)
Strand = Plus / Plus

Query: 643 gattccacagatggcgaggggtgactggagtctctgggtctgtctgcagcgtcacctgcggg 702
|||||
Sbjct: 17955 gattccacagatggcgaggggtgactggagtctctgggtctgtctgcagcgtcacctgcggg
18014

Query: 703 aacggcaaccagaaacggaccgggtcttgtgggtacgcgtgcactgcaacagaatcgagg 762
|||||
Sbjct: 18015 aacggcaaccagaaacggaccgggtcttgtgggtacgcgtgcactgcaacagaatcgagg
18074

Query: 763 acctgtgaccgtccaaactgccagg 788
|||||
Sbjct: 18075 acctgtgaccgtccaaactgccagg 18100

Score = 183 bits (92), Expect = 3e-43
Identities = 92/92 (100%)
Strand = Plus / Plus

Query: 786 aggaattgaagacacttttaggacagctgccaccgaagtgagtctgcttgcggggaagcga 845
|||||
Sbjct: 21788 aggaattgaagacacttttaggacagctgccaccgaagtgagtctgcttgcggggaagcga
21847

Query: 846 ggagtttaatgccaccaaactgtttgaagttg 877
|||||
Sbjct: 21848 ggagtttaatgccaccaaactgtttgaagttg 21879

>AL050320.19.1.107057
Length = 107057

Score = 363 bits (183), Expect = 1e-97
Identities = 183/183 (100%)
Strand = Plus / Plus

Query: 137 agaataacctcaacgtgggaagtgacaccacatcagaaaccagcttttctctctccaaag
196
|||||
Sbjct: 106875 agaataacctcaacgtgggaagtgacaccacatcagaaaccagcttttctctctccaaag
106934

Query: 197 aagcaccaagggagcatctggaccaccaggctgcacaccaacccttccccagaccgcat
256
|||||
Sbjct: 106935 aagcaccaagggagcatctggaccaccaggctgcacaccaacccttccccagaccgcat
106994

Query: 257 tccgacaagagacggggcacccttcattgcaaagagatttccccagatcctttctccttg
316
|||||
Sbjct: 106995 tccgacaagagacggggcacccttcattgcaaagagatttccccagatcctttctccttg
107054

Query: 317 atc 319
|||
Sbjct: 107055 atc 107057

Score = 175 bits (88), Expect = 8e-41
Identities = 88/88 (100%)
Strand = Plus / Plus

Query: 51 cacgctgcacatcacctgtctgcgcgggctcgggagccgccgacggggcccgacgcggccgc 110
|||||
Sbjct: 58200 cacgctgcacatcacctgtctgcgcgggctcgggagccgccgacggggcccgacgcggccgc
58259

Query: 1117 ctgtccctggagagcaccacgctggcgccacagcactgctgctacggcgacaacatgcag 1176

|||||
Sbjct: 28597 ctgtccctggagagcaccacgctggcgccacagcactgctgctacggcgacaacatgcag 28656

Query: 1177 ctcataccaggggcaagggggcgggcacgcccacctcatcagcaccgagttctccgcg 1236

|||||
Sbjct: 28657 ctcataccaggggcaagggggcgggcacgcccacctcatcagcaccgagttctccgcg 28716

Query: 1237 gagctccactacaaggtggacgtcctgccctggattatctgcaaggggtgactggagcagg 1296

|||||
Sbjct: 28717 gagctccactacaaggtggacgtcctgccctggattatctgcaaggggtgactggagcagg 28776

Query: 1297 tataacgaggccccggcctcccaacaacggacagaagtgcacagagagccccctcggacgag 1356

|||||
Sbjct: 28777 tataacgaggccccggcctcccaacaacggacagaagtgcacagagagccccctcggacgag 28836

Query: 1357 gactacatcaagcagttccaagaggccaggggaatattaa 1395

|||||
Sbjct: 28837 gactacatcaagcagttccaagaggccaggggaatattaa 28875

Score = 528 bits (266), Expect = e-147
Identities = 267/268 (99%)
Strand = Plus / Plus

Query: 376 caggtcaccatagaggtgggtcgacggtcctgactctgaagcagataaagatcagcatccg 435

|||||
Sbjct: 9047 caggtcaccatagaggtgggtcgacggtcctgactctgaagcagataaagatcagcatccg 9106

Query: 436 gagaataagcccagctgggtcagtcccatccccgactggcgggcctggtggcagaggtcc 495

|||||
Sbjct: 9107 gagaataagcccagctgggtcagtcccatccccgactggcgggcctggtggcagaggtcc 9166

Query: 496 ctgtccttggccaggggcaaacagcggggaccaggactacragtacgacagtacctcagac 555

|||||
Sbjct: 9167 ctgtccttggccaggggcaaacagcggggaccaggactacaagtacgacagtacctcagac 9226

Query: 556 gacagcaacttcctcaacccccccaggggggtgggaccatacagccccaggccaccggact 615

|||||
Sbjct: 9227 gacagcaacttcctcaacccccccaggggggtgggaccatacagccccaggccaccggact 9286

Query: 111 gggcaacgccagccaagcccagctgcag 138
||||||||||||||||||||
Sbjct: 58260 gggcaacgccagccaagcccagctgcag 58287